

## SEQUENCE LISTING

## (1) GENERAL INFORMATION

(i) APPLICANT: Hillman, Jennifer L.  
 Tang, Y. Tom  
 Corley, Neil C.  
 Guegler, Karl J.  
 Yue, Henry  
 Patterson, Chandra

(ii) TITLE OF THE INVENTION: PROTEINS ASSOCIATED WITH EGF SIGNALING

(iii) NUMBER OF SEQUENCES: 5

## (iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Incyte Genomics, Inc.  
 (B) STREET: 3160 Porter Dr.  
 (C) CITY: Palo Alto  
 (D) STATE: CA  
 (E) COUNTRY: USA  
 (F) ZIP: 94304

## (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette  
 (B) COMPUTER: IBM Compatible  
 (C) OPERATING SYSTEM: DOS  
 (D) SOFTWARE: FastSEQ for Windows Version 2.0

## (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: To Be Assigned  
 (B) FILING DATE: Herewith

## (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 09/069,725  
 (B) FILING DATE: April 29, 1998

## (viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Billings, Lucy J.  
 (B) REGISTRATION NUMBER: 36,749  
 (C) REFERENCE/DOCKET NUMBER: PF-0515-1 CON

## (ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 650-855-0555  
 (B) TELEFAX: 650-845-4166

## (2) INFORMATION FOR SEQ ID NO:1:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 298 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

(A) LIBRARY: COLNNOT16  
 (B) CLONE: 1281694

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Asn Asp Ser Leu Arg Thr Asp Val Phe Val Arg Phe Gln Pro Glu  
 1 5 10 15

Ser Ile Ala Cys Ala Cys Ile Tyr Leu Ala Ala Arg Thr Leu Glu Ile  
 20 25 30  
 Pro Leu Pro Asn Arg Pro His Trp Phe Leu Leu Phe Gly Ala Thr Glu  
 35 40 45  
 Glu Glu Ile Gln Glu Ile Cys Leu Lys Ile Leu Gln Leu Tyr Ala Arg  
 50 55 60  
 Lys Lys Val Asp Leu Thr His Leu Glu Gly Glu Val Glu Lys Arg Lys  
 65 70 75 80  
 His Ala Ile Glu Glu Ala Lys Ala Gln Ala Arg Gly Leu Leu Pro Gly  
 85 90 95  
 Gly Thr Gln Val Leu Asp Gly Thr Ser Gly Phe Ser Pro Ala Pro Lys  
 100 105 110  
 Leu Val Glu Ser Pro Lys Glu Gly Lys Gly Ser Lys Pro Ser Pro Leu  
 115 120 125  
 Ser Val Lys Asn Thr Lys Arg Arg Leu Glu Gly Ala Lys Lys Ala Lys  
 130 135 140  
 Ala Asp Ser Pro Val Asn Gly Leu Pro Lys Gly Arg Glu Ser Arg Ser  
 145 150 155 160  
 Arg Ser Arg Ser Arg Glu Gln Ser Tyr Ser Arg Ser Pro Ser Arg Ser  
 165 170 175  
 Ala Ser Pro Lys Arg Arg Lys Ser Asp Ser Gly Ser Thr Ser Gly Gly  
 180 185 190  
 Ser Lys Ser Gln Ser Arg Ser Arg Ser Arg Ser Asp Ser Pro Pro Arg  
 195 200 205  
 Gln Ala Pro Arg Ser Ala Pro Tyr Lys Gly Ser Glu Ile Arg Gly Ser  
 210 215 220  
 Arg Lys Ser Lys Asp Cys Lys Tyr Pro Gln Lys Pro His Lys Ser Arg  
 225 230 235 240  
 Ser Arg Ser Ser Ser Arg Ser Arg Ser Arg Ser Arg Glu Arg Ala Asp  
 245 250 255  
 Asn Pro Gly Lys Tyr Lys Lys Lys Ser His Tyr Tyr Arg Asp Gln Arg  
 260 265 270  
 Arg Glu Arg Ser Arg Ser Tyr Glu Arg Thr Gly Arg Arg Tyr Glu Arg  
 275 280 285  
 Asp His Pro Gly His Ser Arg His Arg Arg  
 290 295

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3464 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: COLNNOT16
- (B) CLONE: 1281694

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

TTCGTGAAGC	ACTCCATGGA	GCATGTGTCA	ATGGCCTGTG	TCCACCTGGC	TTCCAAGATA	60
GAAGAGGCCC	CAAGACGCAT	ACGGGACGTC	ATCAATGTGT	TTCAACCGCCT	TCGACAGCTG	120
AGAGACAAAA	AATAATCGTT	ATGTACCTTC	AGGTGTTAGA	GTGTGAGCGT	AACCAACACC	180
TGGTCCAGAC	CTCATGGGTA	GCCTCTGAGG	GTAAGTGACT	AAGACTTCTC	CTCTGCTGTC	240
CAAGCGCTTT	GGTGCAGGGA	CAGCGGCATC	TTCAGCCAAT	CCAGTGCAGG	CTCTCCACCG	300
AAGGCTGGCT	CTAGACTGGT	GACCCCTTGT	TGAAATGGGA	CAGTTGGCAG	CGGCTCTGAT	360
GAGCCCAGAG	AGAGGCCTGC	CCTTGGGTGC	GGAGTCTCCC	TCCGCACGAT	GCTCCCACGC	420
GTCCAACCTTG	CACCCAAGGG	GCTTTTCCCT	CTTCCAAGTG	GACTCCTTCA	AGGAAGCTGC	480
AGCTCGGTCA	GCAGAGAAGG	GGCCTGCCGC	CAGCGCCCTG	GAGGAAGAGG	AAGAGGAACC	540
CAAGAGGATG	GCTTGTCTCC	CAGCAGCCAC	ACCGGCTTTG	TGCTCAGCCA	GTTTATTGTA	600
TTTGTGCATG	TTCTCTGCAC	TATGGATTTT	GAGCATTTAG	ATTTCTTTAA	TCAAAAGCGT	660
TTTAGTGACT	CCAGTAGACA	TTTTCTTTCT	GAGGCATCGT	GCTTTGCATG	AGAGCAGGCC	720
AAGGTTGAGG	GGAAAAGTAA	AGTTAAAGTC	GGTTCTCTTT	CATAGCAACA	CGTATTGTCT	780
GACATTCAGC	CAGCTTTTTT	TTTTTCTAAT	AATTTCTGTG	CCTTTCTGTC	CTGTATTTAC	840
TGTATTTAGA	AAAAGCAGCT	AGAATATTTT	TCCATTAACT	CTTGAGATTC	ACAGGACTGT	900

CTAGCTCTGA	GTCCTAGCAA	TAGACTCCTT	AGAGGAGTAG	TACGTTTATC	TAGATTTTCT	960
CTAGATAATG	CAGGCGGAAG	ACCTGGGTTC	CCGGGTGGGG	CATTGCAGTT	CTTCCTGTGT	1020
TTGGCTTCCA	GGAATTACAT	GAACGACAGC	CTTCGCACCG	ACGTCTTCGT	GCGGTTCAG	1080
CCAGAGAGCA	TCGCCGTGTC	CTGCATTTAT	CTTGCTGCCC	GGACGCTGGA	GATCCCTTTG	1140
CCCAATCGTC	CCCATTGGTT	TCTTTTGT	GGAGCAACTG	AAGAAGAAAT	TCAGGAAATC	1200
TGCTTAAAGA	TCTTGCAGCT	TTATGCTCGG	AAAAAGGTTG	ATCTCACACA	CCTGGAGGGT	1260
GAAGTGGAAA	AAAGAAAGCA	CGCTATCGAA	GAGGCAAAGG	CCCAAGCCCC	GGGCTGTGTG	1320
CCTGGGGGCA	CACAGGTGCT	GGATGGTACC	TCGGGGTTCT	CTCCTGCCCC	CAAGCTGGTG	1380
GAATCCCCCA	AAGAAGGTAA	AGGGAGCAAG	CTTCCCCAC	TGTCTGTGAA	GAACACCAAG	1440
AGGAGGCTGG	AGGGCGCCAA	GAAAGCCAAG	GCGGACAGCC	CCGTGAACGG	CTTGCCAAAG	1500
GGGCGAGAGA	GTCGGAGTCG	GAGCCGGAGC	CGTGAGCAGA	GCTACTCGAG	GTCCCCATCC	1560
CGATCAGCGT	CTCCTAAGAG	GAGGAAAAGT	GACAGCGGCT	CCACATCTGG	TGGGTCCAAG	1620
TCGCAGAGCC	GCTCCCGGAG	CAGGAGTGAC	TCCCCACCGA	GACAGGCCCC	CCGACGCGCT	1680
CCCTACAAAG	GCTCTGAGAT	TCGGGGCTCC	CGGAAGTCCA	AGGACTGCAA	GTACCCCCAG	1740
AAGCCACACA	AGTCTCGGAG	CCGGAGTTCT	TCCCGTTCTC	GAAGCAGGTC	ACGGGAGCGG	1800
GCGGATAATC	CGGGAATA	CAAGAAGAAA	AGTCATTACT	ACAGAGATCA	GCGACGAGAG	1860
CGCTCGAGGT	CGTATGAACG	CACAGGCCGT	CGCTATGAGC	GGGACCACCC	TGGGCACAGC	1920
AGGCATCGGA	GGTGAGGCGG	GGTTGCAGTG	ACTGGTGGCC	GCAAGCCCTT	CCCTGGGGAG	1980
TACCTGATGG	CTGCCCTTTG	ACCCCCGGTG	GCTGCCCTTT	GACCCCCGGG	TGTGCTCTCA	2040
GCGCAAGTGG	TCCTAGAACA	GAGATTCTTTT	TGGAATGTCT	TGTCGACTGG	ACCTTGGTGG	2100
ATTTGGAAAT	GGAAGTGGAG	GACCCGTGAC	ACGTGCTTCA	GACCCGTCTG	GGGTGCGGCG	2160
CACACCTGGG	CCCGTGCAGG	GCTCAGCTCG	GCAGCAGCTC	TGAGGGCAGC	TCAATGAAAA	2220
AGTGAATGCA	CACGCCCTTG	TTGGCGTGGC	CTGGCATGGC	CTGGTGCTAT	CGGCAGCCGC	2280
TCTCCACTCC	CCGACTGATA	CTCAATTACG	TGAAGCCAAG	AAAGATGATT	TTTAGAACCT	2340
TTGCCCTATAT	TAGGTTGTAC	TTATGTACAT	ATTTTGCAGT	GTTTCACAGG	AGAAAGTGCG	2400
CTTAAGTGC	CTTATTCTC	TCTCCACGTT	GTAAATAAAC	ATGTGTTTAA	TACAAGTTAA	2460
AGCTATGTAT	GAAAAGTCTC	AAGTTGAATC	CCGTCAGCTT	AAAAGTTGTG	TAGGGAATCC	2520
TGACTTTTAA	AATGTGAGGG	TATTTGGATC	TGTGTTGAAA	GTCGTATATT	TTTATCTGTG	2580
CGGTGCTGAG	TGCAGGCCAC	CAGCTCCTAA	ATAGAGGTTT	CCTATATGCG	CGTATGACAT	2640
GGTGAATAAA	CACAACTCTC	TCCACTCAGG	ACATCCGGAG	CGTTATGGAC	GTGGTAGGTG	2700
GTCGTTCTGT	GTGCTTGTGA	AAGTGTCAG	GCGTGTGCAC	AGCCAGTGCG	CCCACTTCCG	2760
GGCTCCTTGC	TCCCTGCTGT	ACTGAAGTTT	TGGATTTTGC	ATCCAATCCT	GTGTGCCCTGC	2820
CCTTCTGCCG	AAGCTTGTGA	GGGGCCTGAG	TCCTCTGCCC	ATCAGGATGA	CAGGCTCCTT	2880
CCTGCAGGGC	CATAGGAGGG	AAGTTTGGGA	AACACAGAA	GATTCCAAGG	TGCTCTCGTT	2940
CCTGAGGGGG	ACTGGTTTGT	AACCCATGAC	ATCTGTGGGC	GAGAGAGGCA	GCTGGGAGCA	3000
GGACACTTGG	AGGGTCACCC	CACGGGGGTG	GCACCTGCAC	TCTGAGTGCC	CCCCACTGTC	3060
ATCAGCTGCC	TCTTACCGTG	GACACAGTTT	TGGTTTGGG	GACTAGGGGG	CCCCACTCCT	3120
GGTGGTACCG	TTTGGACTTA	CTAGGGCAGT	GGGACATATA	GGCCGGGGCT	AGTGGGATAA	3180
CGGGGAGTTA	CGCCTGATGA	CTTTTGTGAT	GGAATCCTGC	ATTAGATAGC	TGGTGGGACC	3240
CCCCCCTCAG	AATTTGGGGAA	CTGAGGAGAC	TCCAGGGAGG	GTGTCTTCC	AGGGAGAGCA	3300
GCTATGAGGG	GCCCCCTAGC	TTCTGTGCCC	TGGAAGTAAG	AGAACCAGTA	AAGGGCCATA	3360
CACACCTGTA	CCCAAGAGAC	CGCTCTCCAT	TTGCTTTCTT	TTTTTACTAA	ATAATTGTAA	3420
AATATTATTA	TGACATAAAG	AACCATTATA	GGCCAAAAAA	AAAA		3464

## (2) INFORMATION FOR SEQ ID NO:3:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BEPINOT01
- (B) CLONE: 2056178

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Tyr Ser Ala Gln Arg Phe Trp Gly Thr Ile Trp Ala Arg Arg Gly  
 1 5 10 15  
 Ala His Leu Ala Pro Pro Asp Ala Ser Ile Leu Ile Ser Asn Val Cys  
 20 25 30  
 Ser Ile Gly Asp His Val Ala Gln Glu Leu Phe Gln Gly Ser Asp Leu  
 35 40 45  
 Gly Met Ala Glu Glu Ala Glu Arg Pro Gly Glu Lys Ala Gly Gln His  
 50 55 60  
 Ser Pro Leu Arg Glu Glu His Val Thr Cys Val Gln Ser Ile Leu Asp  
 65 70 75 80  
 Glu Phe Leu Gln Thr Tyr Gly Ser Leu Ile Pro Leu Ser Thr Asp Glu  
 85 90 95  
 Val Val Glu Lys Leu Glu Asp Ile Phe Gln Gln Glu Phe Ser Thr Pro  
 100 105 110  
 Ser Arg Lys Gly Leu Val Leu Gln Leu Ile Gln Ser Tyr Gln Arg Met  
 115 120 125  
 Pro Gly Asn Ala Met Val Arg Gly Phe Arg Val Ala Tyr Lys Arg His  
 130 135 140  
 Val Leu Thr Met Asp Asp Leu Gly Thr Leu Tyr Gly Gln Asn Trp Leu  
 145 150 155 160  
 Asn Asp Gln Val Met Asn Met Tyr Gly Asp Leu Val Met Asp Thr Val  
 165 170 175  
 Pro Glu Lys Val His Phe Phe Asn Ser Phe Phe Tyr Asp Lys Leu Arg  
 180 185 190  
 Thr Lys Gly Tyr Asp Gly Val Lys Arg Trp Thr Lys Asn Val Asp Ile  
 195 200 205  
 Phe Asn Lys Glu Leu Leu Leu Ile Pro Ile His Leu Glu Val His Trp  
 210 215 220  
 Ser Leu Ile Ser Val Asp Val Arg Arg Arg Thr Ile Thr Tyr Phe Asp  
 225 230 235 240  
 Ser Gln Arg Thr Leu Asn Arg Arg Cys Pro Lys His Ile Ala Lys Tyr  
 245 250 255  
 Leu Gln Ala Glu Ala Val Lys Lys Asp Arg Leu Asp Phe His Gln Gly  
 260 265 270  
 Trp Lys Gly Tyr Phe Lys Met Asn Val Ala Arg Gln Asn Asn Asp Ser  
 275 280 285  
 Asp Cys Gly Ala Phe Val Leu Gln Tyr Cys Lys His Leu Ala Leu Ser  
 290 295 300  
 Gln Pro Phe Ser Phe Thr Gln Gln Asp Met Pro Lys Leu Arg Arg Gln  
 305 310 315 320  
 Ile Tyr Lys Glu Leu Cys His Cys Lys Leu Thr Val  
 325 330

## (2) INFORMATION FOR SEQ ID NO:4:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1991 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

(A) LIBRARY: BEPINOT01

(B) CLONE: 2056178

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GCCTCCCTGT CCCCCGACCC TCTTTTGTATG CCTCAGCAAG TGAAGAGGAG GAAGAAGAGG 60  
 AGGAGGAGGA GGATGAAGAT GAAGAGGAGG AAGTGGCAGC TTGGAGGCTG CCCCCAAGAT 120  
 GGAGTCAGCT GGGAACCTCC CAGCGGCCCC GCCCTTCCCG CCCACTCAT CGAAAAACCT 180  
 GCTCACAGCG CCGCCGCCGA GCCATGAGAG CTTTCCGGAT GCTGCTCTAC TCAAAAAGCA 240  
 CCTCGCTGAC ATTCCACTGG AAGCTTTGGG GCGGCCACCG GGGCCGCGCG CGGGGCCTCG 300  
 CACACCCCAA GAACCATCTT TCACCCAGC AAGGGGGTGC GACGCCACAG GTGCCATCCC 360  
 CCTGTTGTCTG TTTTGAATCC CCCCAGGGGC CACCTCCACC CCGGCTGGGT CTGCTAGGTG 420  
 CTCTCATGGC TGAGGATGGG GTGAGAGGGT CTCCACCAGT GCCCTCTGGG CCCCCCATGG 480  
 AGGAAGATGG ACTCAGGTGG ACTCCAAAGT CTCCTCTGGA CCTGACTCG GGCCTCCTTT 540  
 CATGTACTCT GCCCAACGGT TTTGGGGGAC AATCTGGGCC AGAAGGGGAG CGCACTTGGC 600  
 ACCCCCTGAT GCCAGCATCC TCATCAGCAA TGTGTGCAGC ATCGGGGACC ATGTGGCCCA 660  
 GGAGCTTTTT CAGGGCTCAG ATTTGGGGCAT GGCAGAAGAG GCAGAGAGGC CTGGGGAGAA 720  
 AGCCGGCCAG CACAGCCCCC TGCAGAGGGA GCATGTGACC TCGGTACAGA GCATCTTGGA 780  
 CGAATTCCTT CAAACGTATG GCAGCCTCAT ACCCCTCAGC ACTGATGAGG TAGTAGAGAA 840  
 GCTGGAGGAC ATTTTCCAGC AGGAGTTTTC CACCCCTTCC AGGAAGGGCC TGGTGTTCGA 900  
 GCTGATCCAG TCTTACCAGC GGATGCCAGG CAATGCCATG GTGAGGGGCT TCCGAGTGGC 960  
 TTATAAGCGG CACGTGCTGA CCATGGATGA CTTGGGGACC TTGTATGGAC AGAACTGGCT 1020  
 CAATGACCAG GTGATGAACA TGTATGGAGA CCTGGTCATG GACACAGTCC CTGAAAAGGT 1080  
 GCATTTCTTC AATAGTTTCT TCTATGATAA ACTCCGTACC AAGGGTTATG ATGGGGTGAA 1140  
 AAGGTGGACC AAAAACGTGG ACATCTTCAA TAAGGAGCTA CTGCTAATCC CCATCCACCT 1200  
 GGAGGTGCAT TGGTCCCTCA TCTCTGTTGA TGTGAGGCGA CGCACCATCA CCTATTTTGA 1260  
 CTCGCAGCGT ACCCTAAACC GCCGCTGCCC TAAGCATATT GCCAAGTATC TACAGGCAGA 1320  
 GCGGTAAAG AAAGACCGAC TGGATTTCCA CCAGGGCTGG AAAGGTACT TCAAAATGAA 1380  
 TGTGGCCAGG CAGAATAATG ACAGTGACTG TGGTGTCTTT GTGTTGCAGT ACTGCAAGCA 1440  
 TCTGGCCCTG TCTCAGCCAT TCAGCTTAC CCAGCAGGAC ATGCCCAAAC TTCGTGGCA 1500  
 GATCTACAAG GAGCTGTGTC ACTGCAAACT CACTGTGTGA GCCTCGTACC CCAGACCCCA 1560  
 AGCCCATAAA TGGGAAGGGA GACATGGGAG TCCCTTCCCA AGAAACTCCA GTTCCTTTCC 1620  
 TCTCTGCCT CTTCCTCATC ACTTCCCTTT GGTTTTTCAT ATTTAAATGT TTCAATTTCT 1680  
 GTATTTTTTT TTCTTTGAGA GAATACTTGT TGATTTCTGA TGTGCAGGGG GTGGCTACAG 1740  
 AAAAGCCCTT TTCTTCTCT GTTTCAGGG GAGTGTGGCC CTGTGGCCTG GGTGGAGCAG 1800  
 TCATCCTCCC CCTTCCCGT GCAGGGAGCA GGAATCAGT GCTGGGGGTG GTGGGCGGAC 1860  
 AATAGGATCA CTGCCTGCCA GATCTTCAAA CTTTATATA TATATATATA TATATATATA 1920  
 TATATATATA TATATATATA TATATATATA AATATATAA TGCCACGGTC CTGCTCTGGT 1980  
 CAATAAAGAT C 1991

## (2) INFORMATION FOR SEQ ID NO:5:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 186 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank  
 (B) CLONE: 1276645

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Glu Gly Pro Lys Lys Ala Gln Gly His Ser Pro Val Asn Gly Leu  
 1 5 10 15  
 Leu Lys Gly Gln Glu Ser Arg Ser Gln Ser Arg Ser Arg Glu Gln Ser  
 20 25 30  
 Tyr Ser Arg Ser Pro Ser Arg Ser Ala Ser Pro Lys Arg Arg Lys Ser  
 35 40 45  
 Asp Ser Gly Ser Thr Ser Gly Gly Ser Lys Ser Gln Ser Arg Ser Arg  
 50 55 60  
 Ser Arg Ser Asp Ser Pro Pro Arg Gln Val His Arg Gly Ala Pro Tyr  
 65 70 75 80  
 Lys Gly Ser Glu Val Arg Gly Ser Arg Lys Ser Lys Asp Cys Lys Tyr  
 85 90 95

PF-0515-1 CON

Leu	Thr	Gln	Lys	Pro	His	Lys	Ser	Arg	Ser	Arg	Ser	Ser	Ser	Arg	Ser
			100					105					110		
Arg	Ser	Arg	Ser	Arg	Glu	Arg	Thr	Asp	Asn	Ser	Gly	Lys	Tyr	Lys	Lys
		115					120					125			
Lys	Ser	His	Tyr	Tyr	Arg	Asp	Gln	Arg	Arg	Glu	Arg	Ser	Arg	Ser	Tyr
		130				135					140				
Glu	Arg	Thr	Gly	His	Arg	Tyr	Glu	Arg	Asp	His	Pro	Gly	His	Ser	Arg
145					150					155					160
His	Arg	Arg	Cys	Asp	Arg	Ile	Ser	Gly	Gly	Cys	Pro	Trp	Ser	Leu	Pro
			165						170					175	
Val	Gly	His	Thr	Leu	Ala	Ser	Val	Ala	Leu						
			180					185							

0304852-050401